

Figure 1

Enzyme E1	Enzyme E2	Number of bases selected in the 5' position	Number of bases selected in the 3' position	Number of potential subgroups (footprints)
<u>Bam H1</u>	+ <u>Mme I</u>	TCCPuAC.....20 AGGPyTG.....18	1/32 (2x4x4) 1/16 (4x4)	16 16
<u>Eco RI</u>	+ <u>Bsm FI</u>10 CCCTG.....14	1/128 (4x2x4x4) 1/16 (4x4)	16 16
<u>Pst I</u>	+ <u>Bsp I</u>	GGGAC.....10 CCCTG.....14	1/256 (4x4x4x4) 1/64 (4x4x4) 1/16 (4x4)	256 256 256
<u>Msp I</u>	+ <u>Xba CI</u>10 CCCCG.....14	1/256 (4x4x4x4) 1/64 (4x4x4) 1/16 (4x4)	256 256 256
<u>Msp I</u>	+ <u>Eci I</u>11 CCCCGA.....11 CCCCCT.....9	1/256 (4x4x4x4) 1/64 (4x4x4) 1/16 (4x4)	16 16 16
<u>Eco 56I</u>	+ <u>Ksp I</u>11 CCCCGG.....11 CCCCCC.....9	1/4 (4)	16

Figure 2

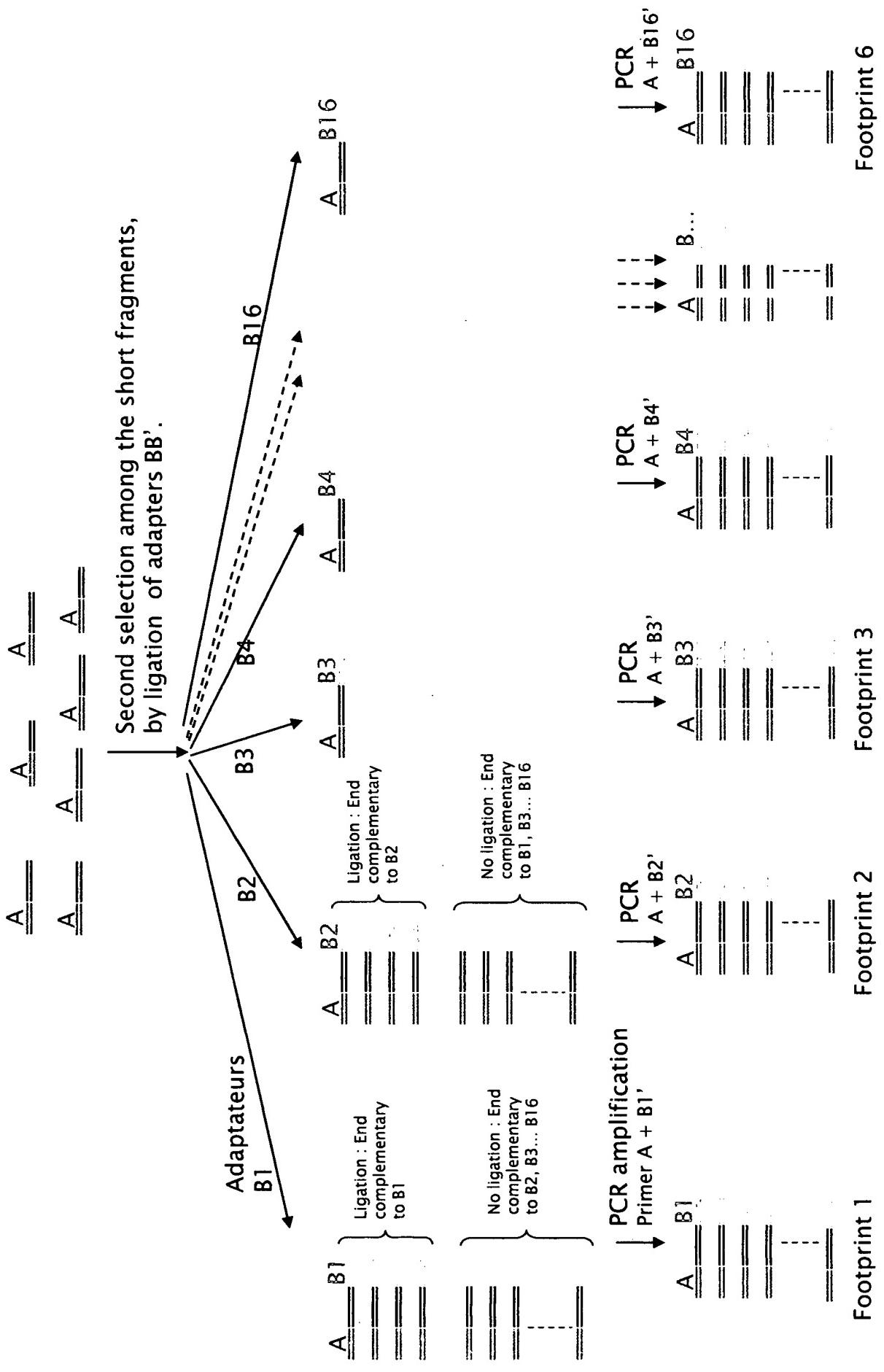


Figure 3

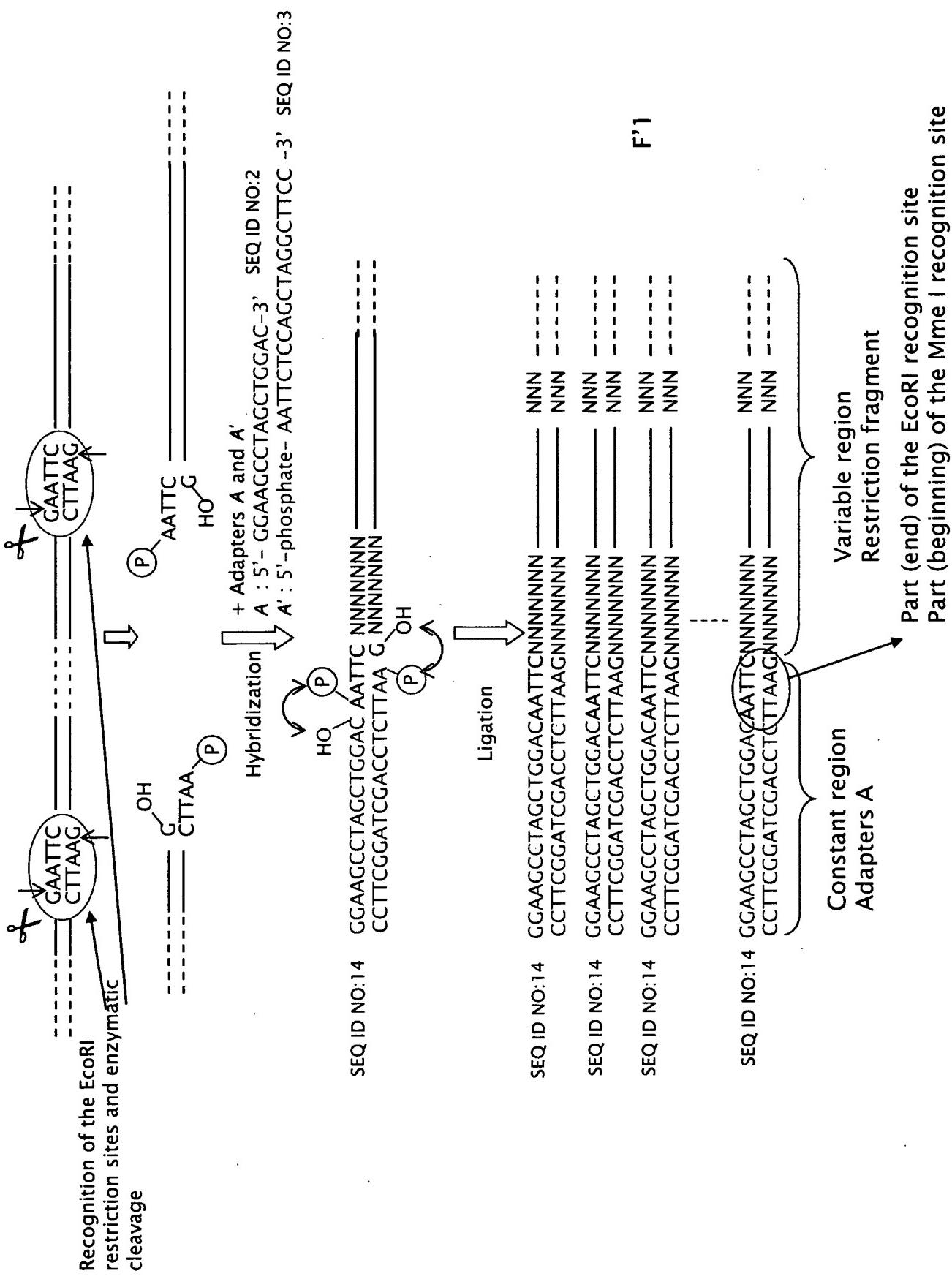


Figure 4-1

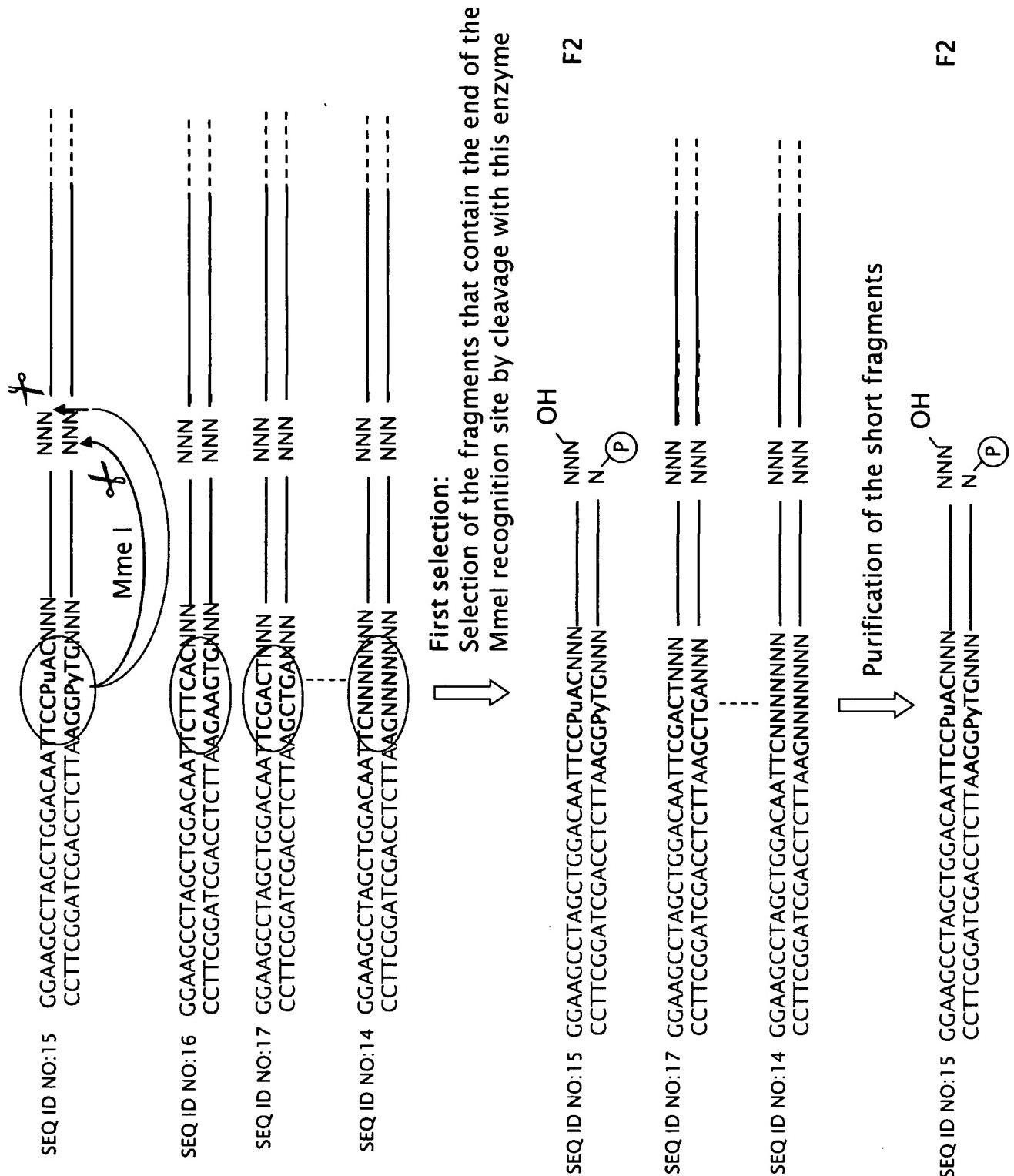


Figure 4-2

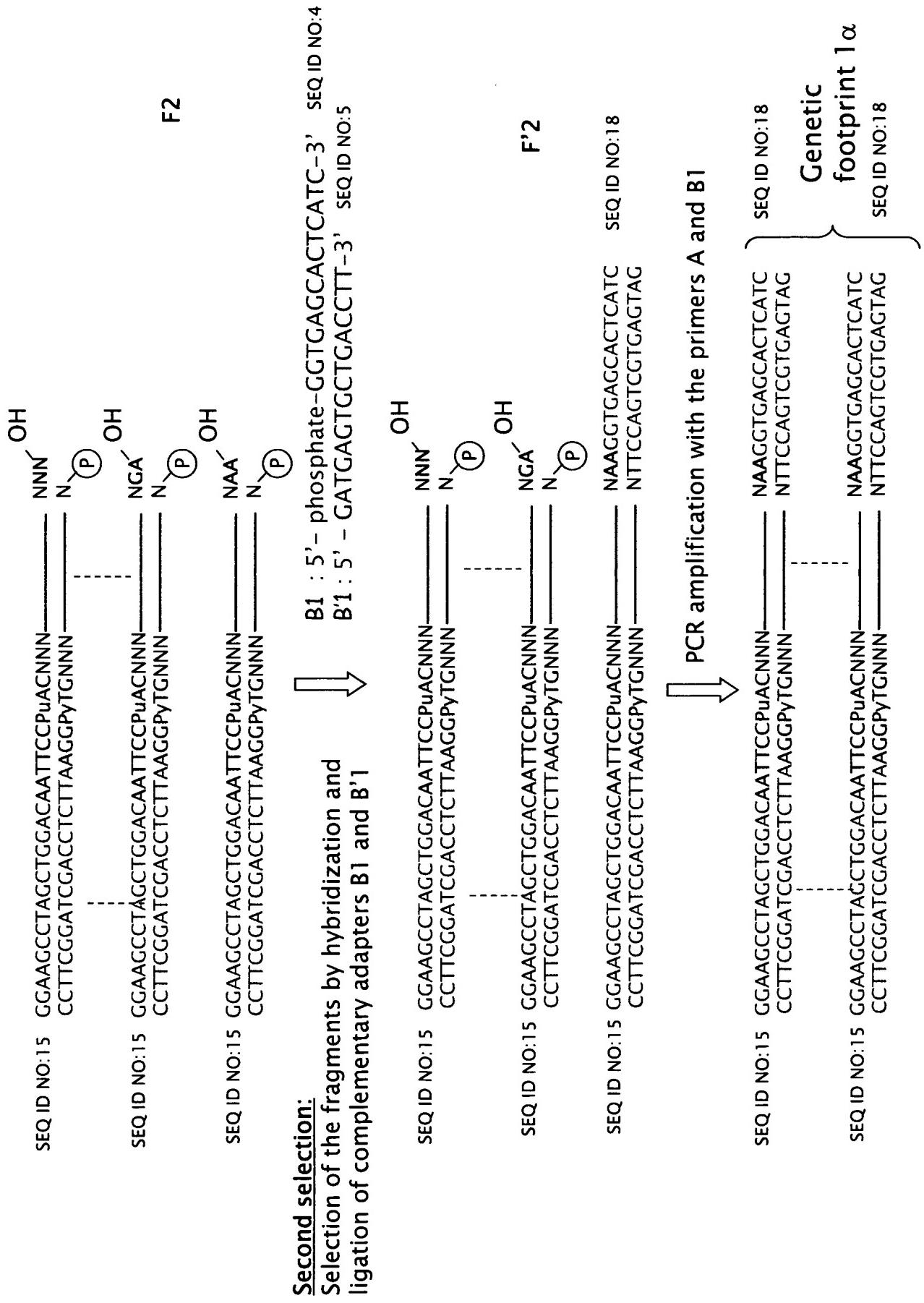


Figure 4-3

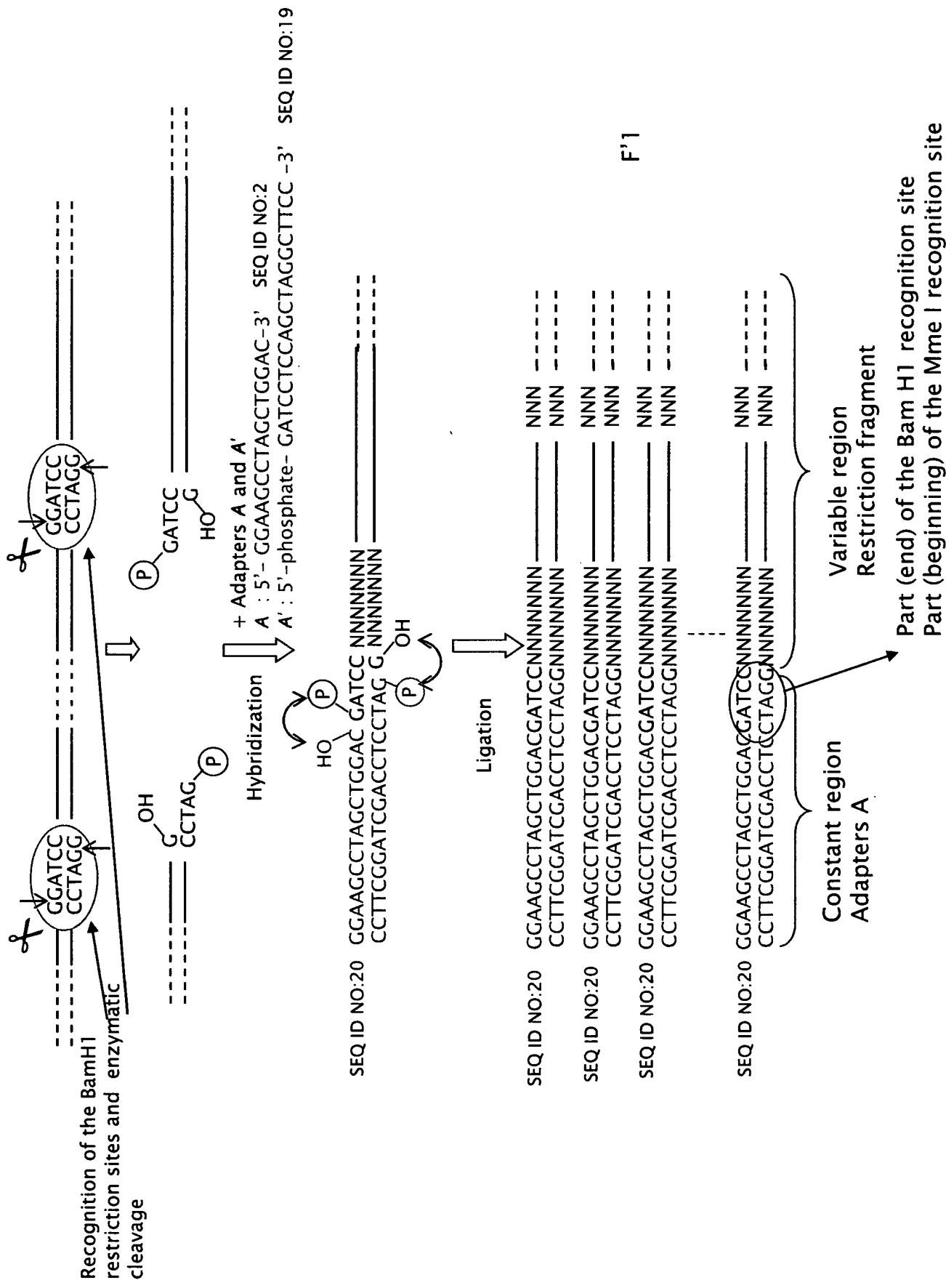


Figure 5-1

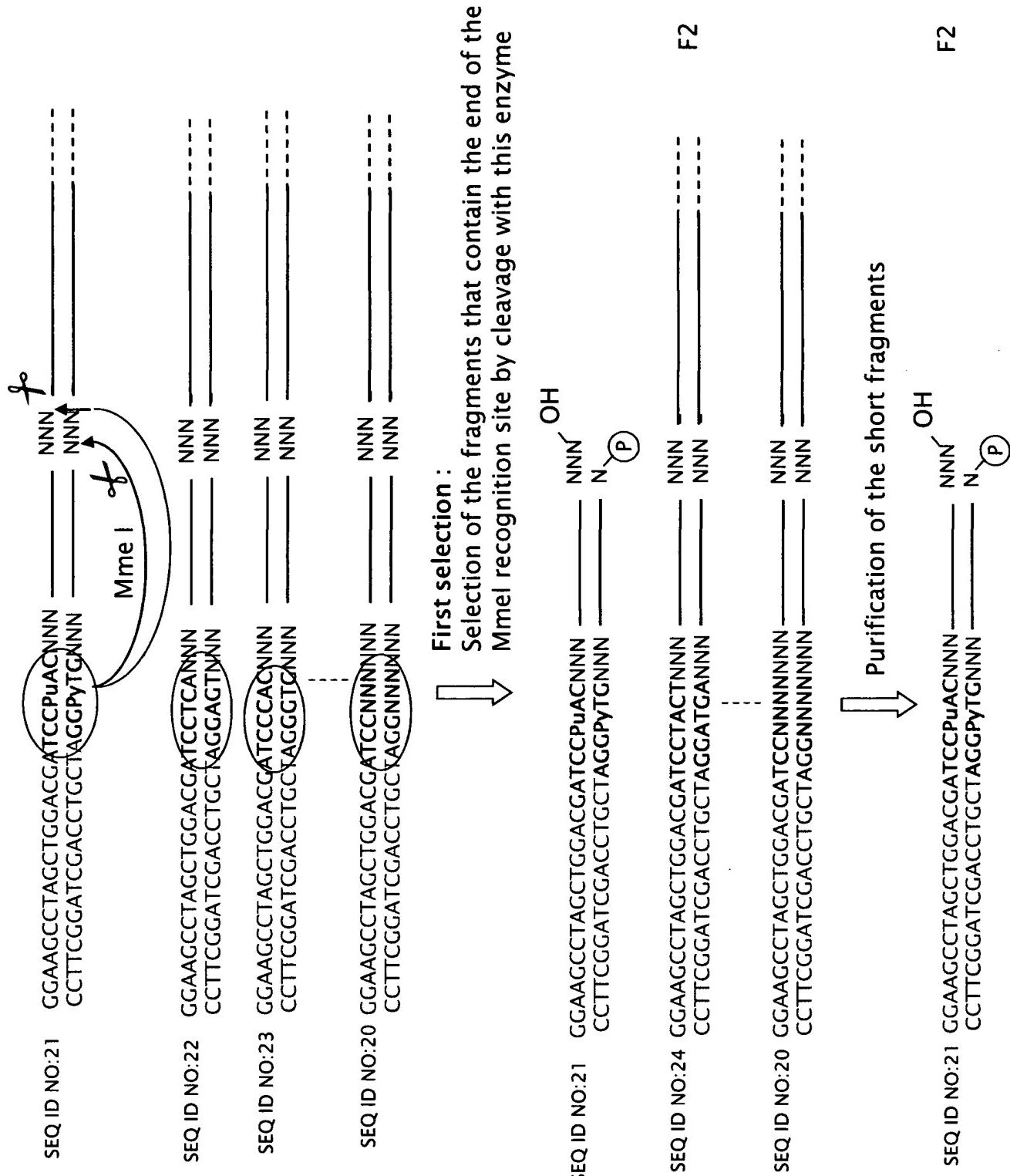


Figure 5-2

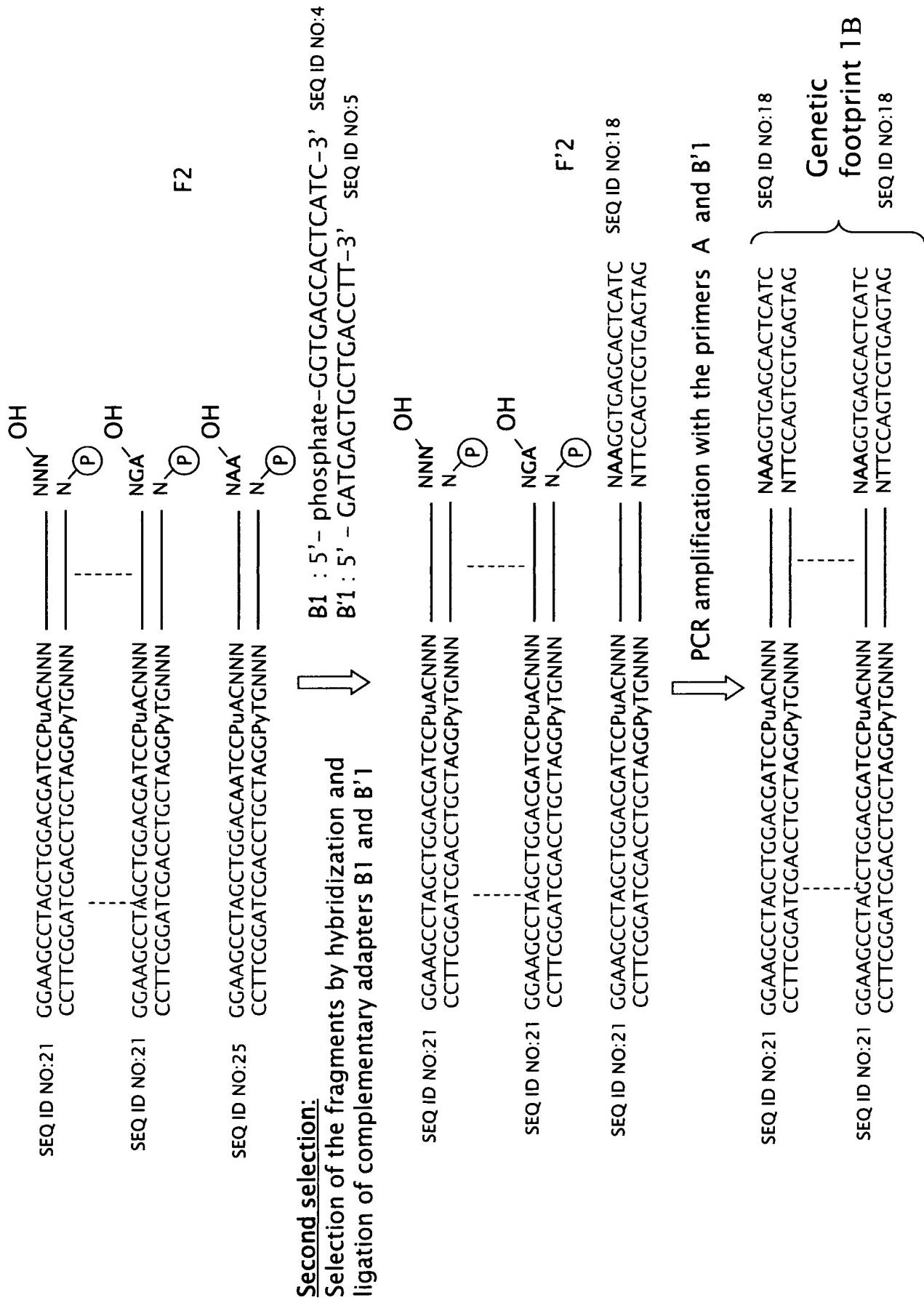


Figure 5-3

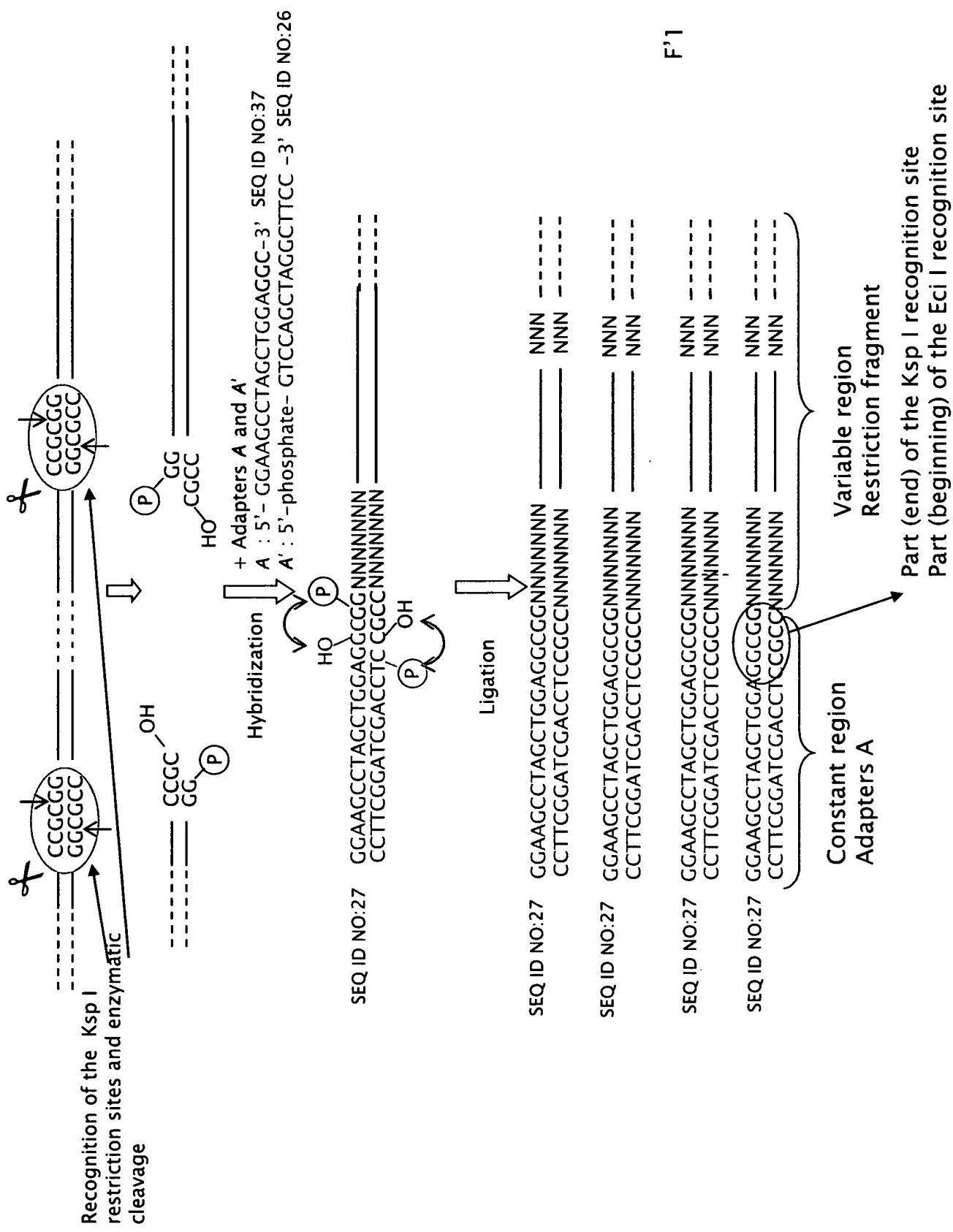


Figure 6-1

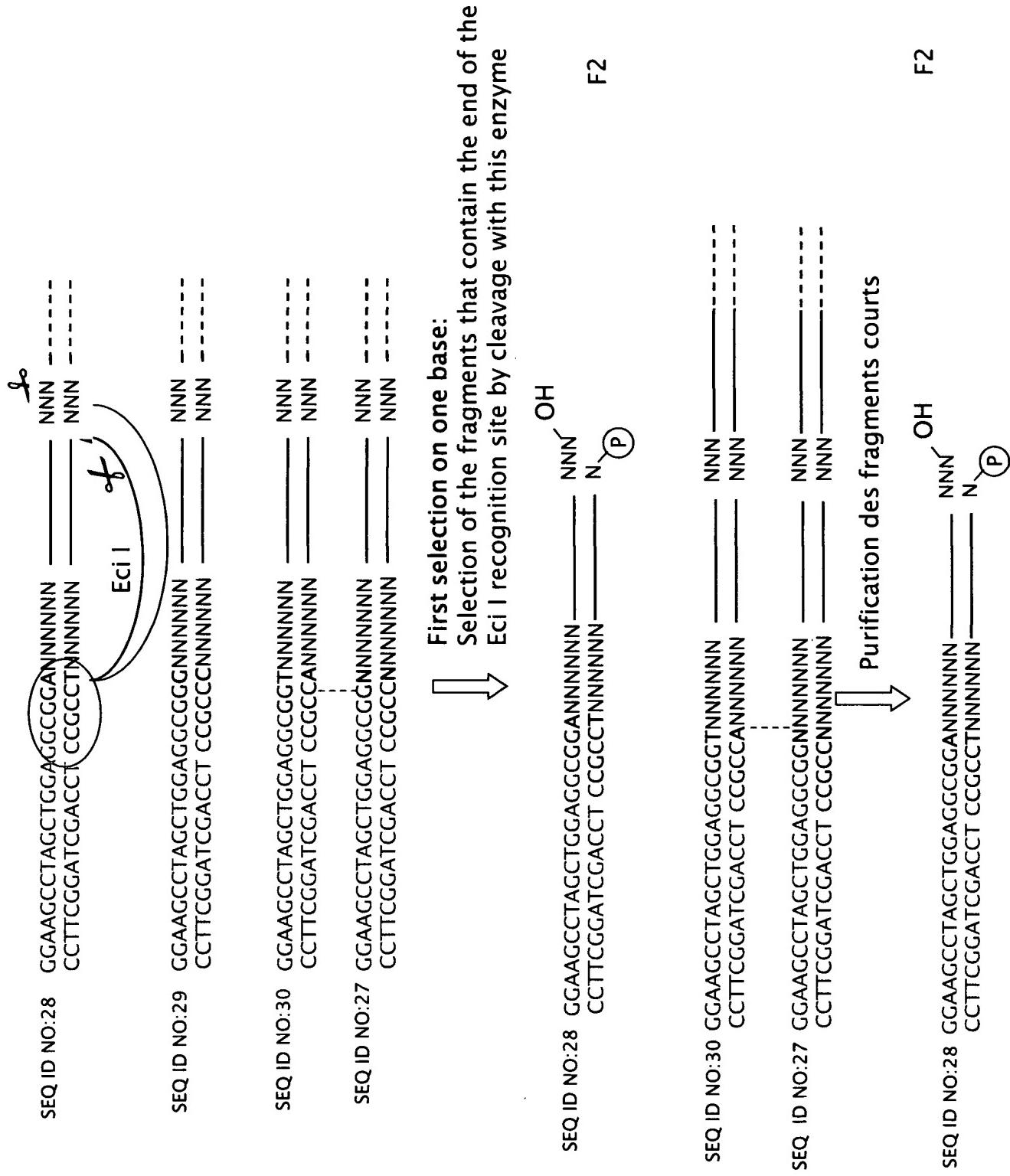


Figure 6-2

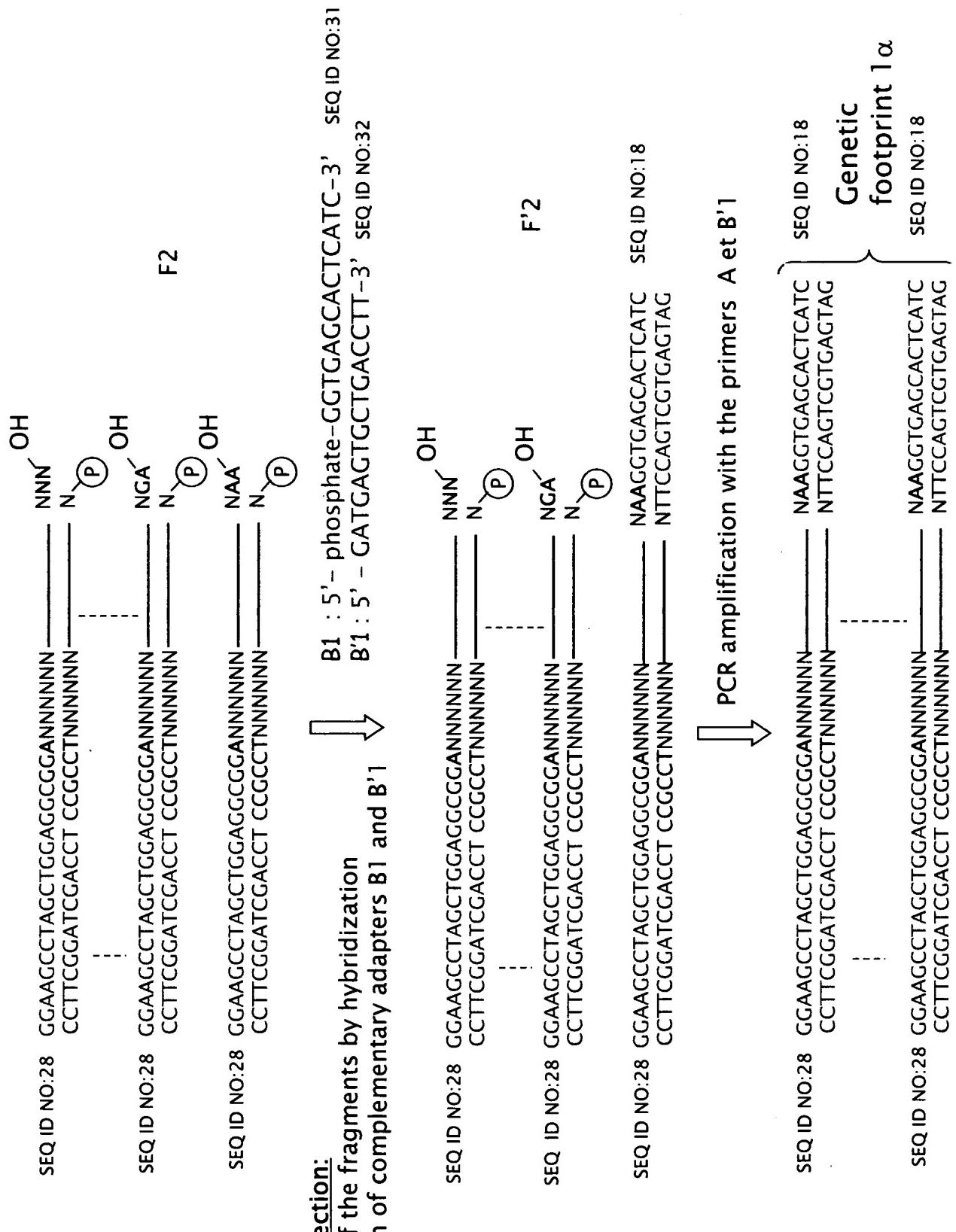


Figure 6-3

7/14

Enzyme E1 _A			Enzyme E2			
Name	Restriction site	Selection 1 of the fragments by cleavage 1 (step a)	Name	Restriction site	Selection 2 of the fragments by cleavage 2 (step c)	Optional selection 3 of the fragments (steps e and f)
<i>Taq^a I</i>	-TCGA -AGCT	governed by E1 _C	<i>BseR I</i>	-GAGGAGN ₁₀ -CTCCTCN ₈ (SEQ ID NO:33)	$\frac{1}{—} = \frac{1}{—}$ $4^4 \quad 256$	$\frac{1}{—} = \frac{1}{—}$ $4^2 \quad 16$
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>BsmF I</i>	-GGGACN ₁₀ -CCCTGN ₁₄ (SEQ ID NO:34)	$\frac{1}{—} = \frac{1}{—}$ $4^3 \quad 64$	$\frac{1}{—} = \frac{1}{—}$ $4^4 \quad 256$
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>Eci I</i>	-GGCGGAN ₁₁ -CCGCCTN ₉ (SEQ ID NO:35)	$\frac{1}{—} = \frac{1}{—}$ $4^4 \quad 256$	$\frac{1}{—} = \frac{1}{—}$ $4^2 \quad 16$
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>Fok I</i>	-GGATGN ₉ -CCTACN ₁₃ (SEQ ID NO:36)	$\frac{1}{—} = \frac{1}{—}$ $4^3 \quad 64$	$\frac{1}{—} = \frac{1}{—}$ $4^4 \quad 256$

Figure 7